

SEQUENCE LISTING

<110> American Home Products

<120> Aggrecanase Molecules

<130> GI5435C

<150> 09/---,---

<151> 2001-10-16

<150> 60/241,469

<151> 2000-10-18

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 242

<212> PRT

<213> Homo sapiens

<400> 1

His Pro Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser Tyr
 1 5 10 15

Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly Phe
 20 25 30

Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu His
 35 40 45

Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His Gln
 50 55 60

Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala Glu
 65 70 75 80

10057487.012500

Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu Val
85 90 95

Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala
100 105 110

Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile
115 120 125

Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr
130 135 140

Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg
145 150 155 160

Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu
165 170 175

Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu
180 185 190

Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly
195 200 205

Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro Arg
210 215 220

Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser Leu
225 230 235 240

Leu Arg

<210> 2

<211> 1045

<212> DNA

<213> Homo sapiens

<400> 2

gaattcggcc aaagaggcct acgagtgtgg tcaggatgga gaggtaggac aggaaggagg 60

gctgaatgcg gagtggggac ggacgtccgg agggctggct ggaagctcgc gcgcccctcc 120

cacggggcgg gcgctacctg agcaggctca gcagctgccg gcggctgcag ggggaccagg 180
cgaggccggc gcggggcgcg gcgccgtccg aagccatcac gtgtccgctg gggccgcagc 240
cgctgccggg cgcgccgtcg tgctccaggc cgaagctgtg cccaatctca tgggcaatgg 300
tgactcccag gtcgaagcca gtgtcctcgg taatgaggca gctccagggt ggggagcagg 360
caccgcccag ctgggtgacg cccgcacact gcgggttacc atcaggcaac tccagggtcaa 420
acctagtgat atagaggacc aggtcagcat ggccaggatc cgtgtcgtcc tcagggttga 480
tggtctggct ccacccacag acgctcagca gggacgagggt gaggttggct gtgatatttg 540
gagcaccctc aggctctgtc agaatgacca tcttcaccag gtgcaccga aactgagccc 600
ccaggggacg gtcccgaagc agttctgccc cgatgttgag gttggtgagc acatagcgct 660
ctgtgtcctc ctgggtgagc tggaagacat cggggccccc gccaccagc agctccagggt 720
gtaggatgcc gcctgcagcc cgcctctgcc tctgcctctg cctctggaag ccagggggaag 780
gagggcgggc ttttaagga gcaccagggc tcaagtaaga agacacggcc tgtggctcca 840
aagcctgaag acaactcggg tgctacacac acagcggccc ccagttccc ttccggcggt 900
cgcatctctc atccccatcc cggatcttgg ggaggtcctc ggcttgcccc agtcaaactc 960
gaggttctcc ctatagttag tcgtattaat ttcagaggag tatttgaag agaagctgaa 1020
gctgtcgaga caaacgaaac tagtg 1045

<210> 3

<211> 1045

<212> DNA

<213> homo sapiens

<400> 3
cactagtttc gtttgtctcg acagcttcag cttctcttct aaatactcct ctgaaattaa 60
tacgactcac tatagggaga acctcgagtt tgactggggc aagccgagga cctccccaag 120
atccgggatg gggatgagag atgcgaacgc cggaaggga ctggggggcc gctgtgtgtg 180
tagcaccoga gttgtcttca ggctttggag ccacaggccg tgtcttctta cttgagccct 240
gggtgtccct taaaaggccg cctccttcc cctggcttcc agaggcagag gcagaggcag 300
aggcgggctg caggcggcat cctacacctg gagctgctgg tggccgtggg ccccgatgtc 360
ttccaggctc accaggagga cacagagcgc tatgtgtctc ccaacctcaa catcggggca 420
gaactgcttc gggaccgctc cctgggggct cagtttcggg tgcacctggt gaagatggtc 480

attctgacag agcctgaggg tgctccaaat atcacagcca acctcacctc gtccctgctg 540
 agcgtctgtg ggtggagcca gaccatcaac cctgaggacg acacggatcc tggccatgct 600
 gacctgggtcc tctatatcac taggtttgac ctggagttgc ctgatggtaa ccggcaggtg 660
 cggggcggtca ccagctggg cgggtgcctgc tccccaacct ggagctgctt cattaccgag 720
 gacactggct tcgacctggg agtcaccatt gcccatgaga ttgggcacag cttcggcctg 780
 gagcacgacg gcgcgcccgg cagcggctgc ggccccagcg gacacgtgat ggcttcggac 840
 ggcgccgcgc ccgcgcgcgg cctcgcttgg tccccctgca gccgcgggca gctgctgagc 900
 ctgctcaggt agcgcgccgc ccgtgggagg ggcgcgcgag cttccagcca gccctccgga 960
 cgtccgtccc cactccgcat tcagccctcc ttcctgtcct acctctccat cctgaccaca 1020
 ctgtaggcc tctttggccg aattc 1045

<210> 4

<211> 2217

<212> DNA

<213> homo sapiens

<400> 4

cagcttcggc ctggagcacg acggcgcgcc cggcagcggc tgccggccca gcggacacgt 60
 gatggcttcg gaacggcgcc gcccgcgcgc ggctcgcct ggtccccctg cagccgcgg 120
 cagctgctga gcctgctcag acccgctcct ccgtcgccgc tccctctgct ggccaccac 180
 ctctgcgcgc gcaggagcct tagtcttggc ccagccaag agccggctcc tgggtggggg 240
 cgcgggccga gaactcctgt tccactcac aaaaggccac gcttccaaac gcttccatcc 300
 tcgtgcccac tctccgtcc cgcctcctcc cgggtgtacac cccgggactg agccgggcct 360
 gagccgggccc ttgtcgcagc gcatgacggg cgcgctggtg tgggaccgc gcgggcctca 420
 acccggttcc gcggggcacc cgcggaatgc gcacctgggc ctctactaca gcgccaacga 480
 gcagtgcgcg gtggccttcg gcccgaaggc tgtgcctgc accttcgcca gggagcacct 540
 ggtgagtctg ccggcgggtg cctgggattg gctgtgaggt cctccgcat caccagctc 600
 acgtcccccc aaacgtgcat ggatatgtgc caggccctct cctgccacac agaccgctg 660
 gaccaaagca gctgcagccg cctcctcgtt cctctcctgg atgggacaga atgtggcgtg 720
 gagaagtggg gctccaaggc tcgctgcgc tccctgggtg agctgacccc catagcagca 780
 gtgcatgggc gctggtctag ctgggggtccc cgaagtcctt gctcccgctc ctgcggagga 840

1057437.042502

```

gggtgtggtca ccaggaggcg gcagtgcaac aaccccagac ctgccttttg ggggcgtgca 900
tgtgttgggtg ctgacctcca ggccgagatg tgcaacactc aggcttgcga gaagaccag 960
ctggagttca tgtcgcaaca gtgcgccagg accgacggcc agccgctgcg ctctccct 1020
ggcggcgct cttctacca ctggggtgct gctgtaccac acagccaagg ggatgctctg 1080
tgcagacaca tgtgccgggc cattggcgag agcttcatca tgaagcgtgg agacagcttc 1140
ctcgatggga cccggtgtat gccaagtggc ccccgaggag acgggacct gagcctgtgt 1200
gtgtcgggca gctgcaggac atttggctgt gatggtagga tggactccca gcaggatgg 1260
gacaggtgcc aggtgtgtgg tggggacaac agcacgtgca gccacggaa gggctctttc 1320
acagctggca gagcgagaga atatgtcacg tttctgacag ttacccccaa cctgaccagt 1380
gtctacattg ccaaccacag gcctctcttc acacacttgg cggtgaggat cggagggcgc 1440
tatgtcgtgg ctgggaagat gagcatctcc cctaacacca cctaccctc cctcctggag 1500
gatggtcgtg tcgagtacag agtggccctc accgaggacc ggctgccccg cctggaggag 1560
atccgcatct ggggacctt ccaggaagat gctgacatcc aggtgggagg tgtcagagcc 1620
cagctcatgc acatcagctg gtggagcagg cctggccttg gagaacgaga cctgtgtgcc 1680
aggggcagat ggcttgagg ctccagtgc tgaggggcct ggctccgtag atgagaagct 1740
gcctgcccc ctgacctgtg tcgggatgtc atgtcctcca ggctggggcc atctggatgc 1800
cacctctgca ggggagaagg ctccctccc atggggcagc atcaggacgg gggctcaagc 1860
tgcacacgtg tggaccttg cggcagggtc gtgtccgtc tctgcgggc gaggtctgat 1920
ggagctgcgt ttctgtgca tggactctgc cctcagggtg cctgtccagg aagagctgtg 1980
tggcctggca agcaagcctg ggagccggcg ggaggtctgc caggtgtcc cgtgccctgc 2040
tcggtggcag tacaagctgg cggcctgcag cgtgagctgt gggagagggg tcgtgcggag 2100
gatcctgtat tgtgccggg cccatgggga ggacgatggt gaggagatcc tgttgacac 2160
ccagtgccag gggctgcctc gcccggaacc ccaggaggcc tgcagcctgg agccctg 2217

```

<210> 5

<211> 365

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (365)..(365)

<223> unknown amino acid

<400> 5

Met Asp Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln
1 5 10 15

Ser Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys
20 25 30

Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val Glu
35 40 45

Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp Gly Pro
50 55 60

Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg
65 70 75 80

Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val
85 90 95

Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys
100 105 110

Thr Gln Leu Glu Phe Met Ser Gln Gln Cys Ala Arg Thr Asp Gly Gln
115 120 125

Pro Leu Arg Ser Ser Pro Gly Gly Ala Ser Phe Tyr His Trp Gly Ala
130 135 140

Ala Val Pro His Ser Gln Gly Asp Ala Leu Cys Arg His Met Cys Arg
145 150 155 160

Ala Ile Gly Glu Ser Phe Ile Met Lys Arg Gly Asp Ser Phe Leu Asp
165 170 175

Gly Thr Arg Cys Met Pro Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser
180 185 190

Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met
195 200 205

Asp Ser Gln Gln Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn
210 215 220

Ser Thr Cys Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg
225 230 235 240

Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
245 250 255

Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
260 265 270

Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr Thr
275 280 285

Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val Ala Leu
290 295 300

Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro
305 310 315 320

Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu
325 330 335

Met His Ile Ser Trp Trp Ser Arg Pro Gly Leu Gly Glu Arg Asp Leu
340 345 350

Cys Ala Arg Gly Arg Trp Pro Gly Gly Ser Ser Asp Xaa
355 360 365

<210> 6

<211> 738

<212> PRT

<213> homo sapien

<220>

<221> MISC_FEATURE

<222> (43)..(43)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (192)..(192)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (255)..(255)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (258)..(258)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (374)..(374)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (397)..(397)

<223> unknown amino acid

<220>

2025-04-20 10:54:23

<221> MISC_FEATURE

<222> (452)..(452)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (458)..(458)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (475)..(475)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (487)..(487)

<223> unknown amino acid

<400> 6

Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly Cys Gly Pro
1 5 10 15

Ser Gly His Val Met Ala Ser Glu Arg Arg Arg Pro Ala Pro Ala Ser
20 25 30

Pro Gly Pro Pro Ala Ala Ala Gly Ser Cys Xaa Ala Cys Ser Asp Pro
35 40 45

Ser Leu Arg Arg Arg Ser Leu Cys Trp Pro Pro Thr Ser Ala Pro Ala
50 55 60

Gly Ala Leu Val Leu Val Pro Ala Lys Ser Arg Leu Leu Val Gly Gly
65 70 75 80

Ala Gly Arg Glu Leu Leu Phe Pro Leu Thr Lys Gly His Ala Ser Lys
85 90 95

Arg Phe His Pro Arg Ala His Ser Ser Val Pro Pro Pro Gly Val
100 105 110

His Pro Gly Thr Glu Pro Gly Leu Ser Arg Ala Leu Ser Gln Arg Met
115 120 125

Thr Gly Ala Leu Val Trp Asp Pro Pro Arg Pro Gln Pro Gly Ser Ala
130 135 140

Gly His Pro Arg Asn Ala His Leu Gly Leu Tyr Tyr Ser Ala Asn Glu
145 150 155 160

Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val Ala Cys Thr Phe Ala
165 170 175

Arg Glu His Leu Val Ser Leu Pro Ala Val Ala Trp Asp Trp Leu Xaa
180 185 190

Gly Pro Ser Ala Ser Pro Ser Ser Arg Pro Pro Lys Arg Ala Trp Ile
195 200 205

Cys Ala Arg Pro Ser Pro Ala Thr Gln Thr Arg Trp Thr Lys Ala Ala
210 215 220

Ala Ala Ala Ser Ser Phe Leu Ser Trp Met Gly Gln Asn Val Ala Trp
225 230 235 240

Arg Ser Gly Ala Pro Arg Val Ala Ala Ala Pro Trp Trp Ser Xaa Pro
245 250 255

Pro Xaa Gln Gln Cys Met Gly Ala Gly Leu Ala Gly Val Pro Glu Val
260 265 270

Leu Ala Pro Ala Pro Ala Glu Glu Val Trp Ser Pro Gly Gly Gly Ser
275 280 285

Ala Thr Thr Pro Asp Leu Pro Leu Gly Gly Val His Val Leu Val Leu
290 295 300

Thr Ser Arg Pro Arg Cys Ala Thr Leu Arg Pro Ala Arg Arg Pro Ser
305 310 315 320

205270-28425001

Trp Ser Ser Cys Arg Asn Ser Ala Pro Gly Pro Thr Ala Ser Arg Cys
325 330 335

Ala Pro Pro Leu Ala Ala Pro Pro Ser Thr Thr Gly Val Leu Leu Tyr
340 345 350

His Thr Ala Lys Gly Met Leu Cys Ala Asp Thr Cys Ala Gly Pro Leu
355 360 365

Ala Arg Ala Ser Ser Xaa Ser Val Glu Thr Ala Ser Ser Met Gly Pro
370 375 380

Gly Val Cys Gln Val Ala Pro Gly Arg Thr Gly Pro Xaa Ala Cys Val
385 390 395 400

Cys Arg Ala Ala Ala Gly His Leu Ala Val Met Val Gly Trp Thr Pro
405 410 415

Ser Arg Tyr Gly Thr Gly Ala Arg Cys Val Val Gly Thr Thr Ala Arg
420 425 430

Ala Ala His Gly Arg Ala Leu Ser Gln Leu Ala Glu Arg Glu Asn Met
435 440 445

Ser Arg Phe Xaa Gln Leu Pro Pro Thr Xaa Pro Val Ser Thr Leu Pro
450 455 460

Thr Thr Gly Leu Ser Ser His Thr Trp Arg Xaa Gly Ser Glu Gly Ala
465 470 475 480

Met Ser Trp Leu Gly Arg Xaa Ala Ser Pro Leu Thr Pro Pro Thr Pro
485 490 495

Pro Ser Trp Arg Met Val Val Ser Ser Thr Glu Trp Pro Ser Pro Arg
500 505 510

Thr Gly Cys Pro Ala Trp Arg Arg Ser Ala Ser Gly Asp Pro Ser Arg
515 520 525

Lys Met Leu Thr Ser Arg Trp Glu Val Ser Glu Pro Ser Ser Cys Thr
530 535 540

Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val Pro
545 550 555 560

Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser Val
565 570 575

Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys Pro
580 585 590

Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro
595 600 605

Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp
610 615 620

Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met
625 630 635 640

Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln
645 650 655

Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val
660 665 670

Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala Ala
675 680 685

Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr Cys
690 695 700

Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp Thr
705 710 715 720

Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser Leu
725 730 735

Glu Pro

<210> 7

<211> 4284

<212> DNA

<213> homo sapien

<400> 7

atgcaccagc gtcacccctg ggcaagatgc cctccccctct gtgtggcccg aatccttgcc	60
tgtggctttc tcttgggctg ctggggaccc tcccatttcc agcagagttg tcttcaggct	120
ttggagccac aggcogtgtc ttcttacttg agccctgggtg ctcccttaaa aggccgcct	180
ccttccccctg gcttccagag gcagaggcag aggcagaggc gggctgcagg cggcatccta	240
cacctggagc tgctgggtggc cgtggggcccc gatgtcttcc aggctcacca ggaggacaca	300
gagcgctatg tgctcaccaa cctcaacatc ggggcagaac tgcttcggga cccgtccctg	360
ggggctcagt ttcgggtgca cctgggtgaag atggtcattc tgacagagcc tgaggggtgcc	420
ccaaatatca cagccaacct cacctcgtcc ctgctgagcg tctgtgggtg gagccagacc	480
atcaaccctg aggacgacac ggatcctggc catgctgacc tggtcctcta tatcactagg	540
tttgacctgg agttgcctga tggtaacggc caggtgctgg gcgtcaccca gctgggcggt	600
gcctgctccc caacctggag ctgcctcatt accgaggaca ctggcttcga cctgggagtc	660
accattgccc atgagattgg gcacagcttc ggcttgagc acgacggcgc gcccggcagc	720
ggctgcggcc ccagcggaca cgtgatggct tcggacggcg ccgcgccccg cgcgggcctc	780
gcctggctccc cctgcagccg ccggcagctg ctgagcctgc tcagcgcagg acgggcgcgc	840
tgctgttggg acccgccgcg gcctcaaccc gggtcgcggg ggcacccgcc ggatgcgcag	900
cctggcctct actacagcgc caacgagcag tgccgcgtgg ccttcggccc caaggctgtc	960
gcctgcacct tcgccaggga gcacctggat atgtgccagg ccctctcctg ccacacagac	1020
ccgctggacc aaagcagctg cagccgcctc ctogttcctc tccctggatgg gacagaatgt	1080
ggcgtggaga agtgggtgctc caagggtcgc tgccgctccc tgggtggagct gacccccata	1140
gcagcagtg c atgggcgctg gtctagctgg ggtccccgaa gtccttgctc ccgctcctgc	1200
ggaggaggtg tggtcaccag gaggcggcag tgcaacaacc ccagadctgc ctttgggggg	1260
cgtgcatgtg ttggtgctga cctccaggcc gagatgtgca aactcaggc ctgcgagaag	1320
accagctgg agttcatgtc gcaacagtg gccaggaccg acggccagcc gctgcgctcc	1380
tcccctggcg gcgcctcctt ctaccactgg ggtgctgctg taccacacag ccaaggggat	1440
gctctgtgca gacacatgtg ccgggccatt ggcgagagct tcatcatgaa gcgtggagac	1500
agcttcctcg atgggacccg gtgtatgcca agtggccccc gggaggacgg gaccctgagc	1560
ctgtgtgtgt cgggcagctg caggacattt ggctgtgatg gtaggatgga ctcccagcag	1620
gtatgggaca ggtgccagggt gtgtgggtggg gacaacagca cgtgcagccc acggaagggc	1680
tctttcacag ctggcagagc gagagaatat gtcacgtttc tgacagttac cccaacctg	1740
accagtgtct acattgccaa ccacaggcct ctcttcacac acttggcggt gaggatcgga	1800

ggcgctatg tctgtggtgg gaagatgagc atctccccta acaccaccta cccctccctc	1860
ctggaggatg gtcgtgtcga gtacagagtg gccctcaccg aggaccggct gccccgcctg	1920
gaggagatcc gcatctgggg acccctccag gaagatgctg acatccaggt ttacaggcgg	1980
tatggcgagg agtatggcaa cctcaccgc ccagacatca cttcaccta cttccagcct	2040
aagccacggc aggctgggt gtgggccgct gtgctgggc cctgctcggg gagctgtggg	2100
gcagggctgc gctgggtaaa ctacagctgc ctggaccagg ccaggaagga gttggtggag	2160
actgtccagt gccaaggag ccagcagcca ccagcgtggc cagaggcctg cgtgctcga	2220
ccctgccctc cctactgggc ggtgggagac ttcgggccat gcagcgctc ctgtgggggc	2280
ggcctgcggg agcgccagt gcgctgcgtg gaggcccagg gcagcctcct gaagacattg	2340
ccccagccc ggtgcagagc aggggcccag cagccagctg tggcgctgga aacctgcaac	2400
ccccagccct gccctgccag gtgggaggtg tcagagccca gctcatgcac atcagctggt	2460
ggagcaggcc tggccttga gaacgagacc tgtgtgccag gggcagatgg cctggaggct	2520
ccagtactg aggggcctgg ctccgtagat gagaagctgc ctgcccctga gccctgtgtc	2580
gggatgtcat gtccctcagg ctggggccat ctggatgcc cctctgcagg ggagaaggct	2640
ccctcccat ggggcagcat caggacggg gctcaagctg cacacgtgtg gaccctgcg	2700
gcagggctgt gctccgtctc ctgcgggcca ggtctgatgg agctgcgtt cctgtgcatg	2760
gactctgccc tcagggtgcc tgtccaggaa gagctgtgtg gcctggcaag caagcctggg	2820
agccggcggg aggtctgcca ggctgtccc tgccctgctc ggtggcagta caagctggcg	2880
gcctgcagcg tgagctgtgg gagaggggtc gtgcggagga tcctgtattg tgccggggcc	2940
catggggagg acgatggtga ggagatcctg ttggacaccc agtgccaggg gctgcctcgc	3000
ccggaacccc aggaggcctg cagcctggag ccctgcccac ctagggtgaa agtcatgtcc	3060
cttgggccat gttcggccag ctgtggcctt ggcaactgcta gacgctcggg ggctgtgtg	3120
cagctcgacc aaggccagga cgtggaggtg gacgaggcg cctgtgcggc gctggtgcgg	3180
cccaggcca gtgtcccctg tctcattgcc gactgcacct accgctggca tgttggcacc	3240
tggatggagt gctctgtttc ctgtggggat ggcattccag gccggcgtga cacctgcctc	3300
ggaccccagg cccaggcgcc tgtgccagct gatttctgcc agcacttgcc caagccggtg	3360
actgtgcgtg gctgctgggc tgggccctgt gtgggacagg gtacgccag cctggtgccc	3420
cacgaagaag ccgctgctcc aggacggacc acagccaccc ctgctggtgc ctccctggag	3480
tgggccagg cccggggcct gctcttctcc ccggtcccc agcctcggcg gctcctgccc	3540
gggccccagg aaaactcagt gcagtccagt gcctgtggca ggcagcacct tgagccaaca	3600

ggaaccattg acatgcgagg cccagggcag gcagactgtg cagtggccat tgggcggccc 3660
 ctcggggagg tgggtgaccct ccgcgtcctt gagagttctc tcaactgcag tgcgggggac 3720
 atgttgctgc tttggggccg gctcacctgg aggaagatgt gcaggaagct gttggacatg 3780
 acttttcagct ccaagaccaa cacgctggtg gtgaggcagc gctgcgggcg gccaggaggt 3840
 ggggtgctgc tgcggtatgg gagccagctt gctcctgaaa ccttctacag agaatgtgac 3900
 atgcagctct ttgggccctg gggtgaaatc gtgagcccct cgctgagtcc agccacgagt 3960
 aatgcagggg gctgccggct cttcattaat gtggctccgc acgcacggat tgccatccat 4020
 gccctggcca ccaacatggg cgctgggacc gagggagcca atgccagcta catcttgatc 4080
 cgggacaccc acagcttgag gaccacagcg ttccatgggc agcaggtgct ctactgggag 4140
 tcagagagca gccaggctga gatggagttc agcgagggct tccatgaaggc tcaggccagc 4200
 ctgcggggcc agtactggac cctccaatca tgggtaccgg agatgcagga ccctcagtcc 4260
 tggaagggaa aggaaggaac ctga 4284

<210> 8

<211> 1427

<212> PRT

<213> homo sapiens

<400> 8

Met His Gln Arg His Pro Trp Ala Arg Cys Pro Pro Leu Cys Val Ala
 1 5 10 15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
 20 25 30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
 35 40 45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
 50 55 60

Phe Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
 65 70 75 80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
 85 90 95

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
100 105 110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
115 120 125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
130 135 140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145 150 155 160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
165 170 175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
180 185 190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
195 200 205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
210 215 220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225 230 235 240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
245 250 255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
260 265 270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
275 280 285

Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
290 295 300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305 310 315 320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
325 330 335

Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
340 345 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
355 360 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
370 375 380

Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385 390 395 400

Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
405 410 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
420 425 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
435 440 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
450 455 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465 470 475 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
485 490 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
500 505 510

Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
515 520 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
530 535 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545 550 555 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
565 570 575

1057437-01500

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
580 585 590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
595 600 605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
610 615 620

Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625 630 635 640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
645 650 655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
660 665 670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
675 680 685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
690 695 700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705 710 715 720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
725 730 735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
740 745 750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
755 760 765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
770 775 780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785 790 795 800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
805 810 815

Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
820 825 830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
835 840 845

Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
850 855 860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865 870 875 880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
885 890 895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
900 905 910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
915 920 925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
930 935 940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945 950 955 960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
965 970 975

Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
980 985 990

Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser
995 1000 1005

Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser Leu Gly Pro
1010 1015 1020

Cys Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg Ser Val Ala
1025 1030 1035

Cys Val Gln Leu Asp Gln Gly Gln Asp Val Glu Val Asp Glu Ala
1040 1045 1050

Ala Cys Ala Ala Leu Val Arg Pro Glu Ala Ser Val Pro Cys Leu
1055 1060 1065

Ile Ala Asp Cys Thr Tyr Arg Trp His Val Gly Thr Trp Met Glu
1070 1075 1080

Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg Arg Asp Thr
1085 1090 1095

Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala Asp Phe Cys
1100 1105 1110

Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys Trp Ala Gly
1115 1120 1125

Pro Cys Val Gly Gln Gly Thr Pro Ser Leu Val Pro His Glu Glu
1130 1135 1140

Ala Ala Ala Pro Gly Arg Thr Thr Ala Thr Pro Ala Gly Ala Ser
1145 1150 1155

Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu Phe Ser Pro Ala Pro
1160 1165 1170

Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu Asn Ser Val Gln
1175 1180 1185

Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr Gly Thr Ile
1190 1195 1200

Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val Ala Ile Gly
1205 1210 1215

Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu Glu Ser Ser
1220 1225 1230

Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp Gly Arg Leu
1235 1240 1245

Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met Thr Phe Ser
1250 1255 1260

Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys Gly Arg Pro
1265 1270 1275

Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu Ala Pro Glu
1280 1285 1290

Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe Gly Pro Trp Gly
1295 1300 1305

Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser Asn Ala Gly
1310 1315 1320

Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala Arg Ile Ala
1325 1330 1335

Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr Glu Gly Ala
1340 1345 1350

Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser Leu Arg Thr
1355 1360 1365

Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu Ser Glu Ser
1370 1375 1380

Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu Lys Ala Gln
1385 1390 1395

Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser Trp Val Pro
1400 1405 1410

Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu Gly Thr
1415 1420 1425

10057427.012202